

08/320157

Figure 1

bcl Consensus PCR Primers

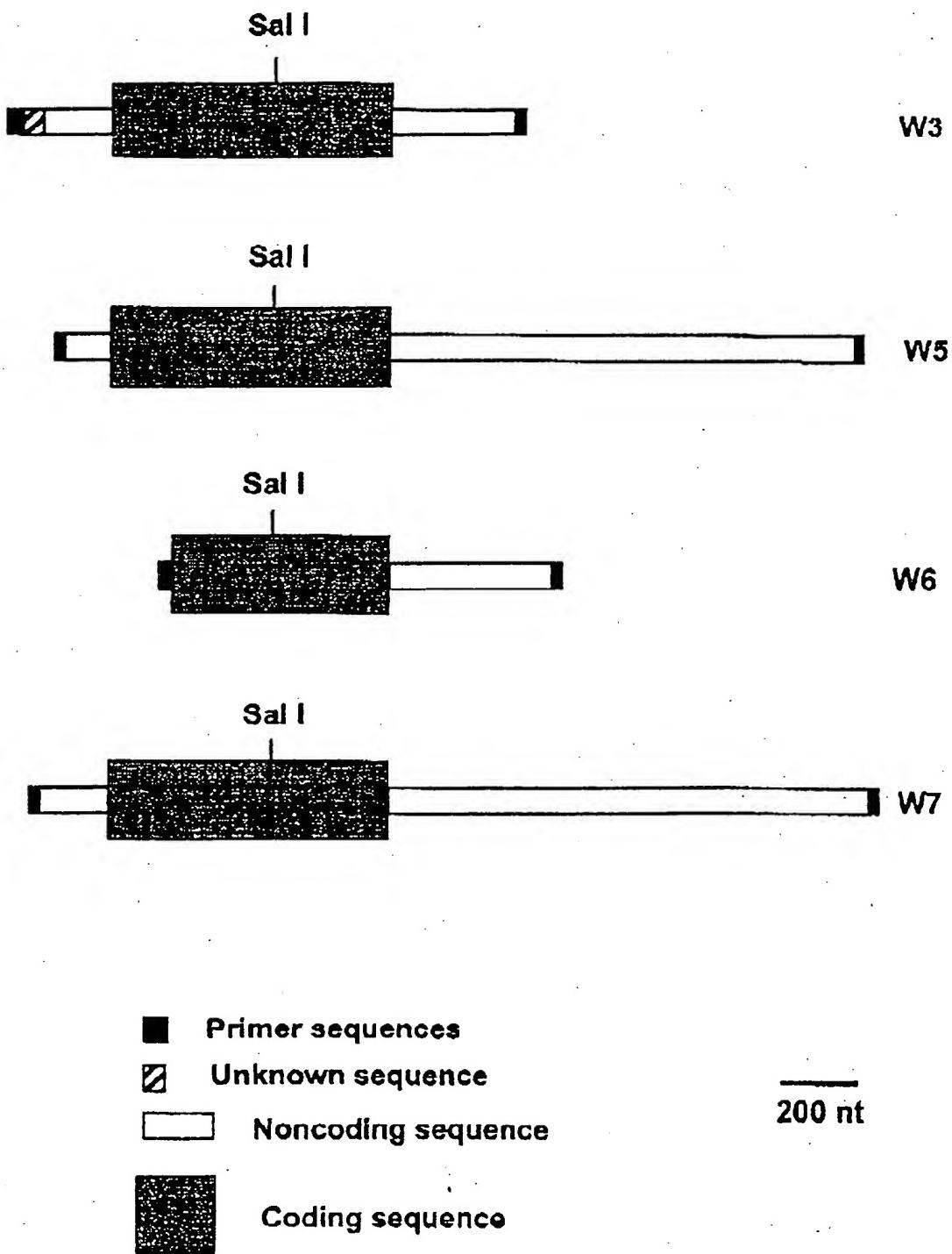
Ile
EcoRI AspTrpGlyArgValValAla
5- AGATCTGAATTCAACTTGGGGGIC(A)GIA(G)TXGTXGC -3' bclx 1-32

AspTrpGlyGlyGlnGluAsnAspGlnIleTrp
AGGGTIGGIGGXACXAGA(G)ACA(T)(C)TAGGT
5'- AGATCT'AAGCTTGTCCAIICCICCGXTGCC(T)TGA(G)ATCCA -3' bclx 2-39

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Figure 2

Cdi-1 cDNA clones



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Figure 3

10 * 20 * 30 * 40 *

GAG GAT CTA CAG GGG ACA AGT AAA GGC TAC ATC CAG ATG CCG GGA ATG
CTC CTA GAT GTC CCC TGT TCA TTT CGG ATG TAG GTC TAC GGC CCT TAC

>Aha2

50 | 60 * 70 * 80 * 90 *

CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC CCA CTC AGC CCC TGG GAG
GTC ACT GCG GGT AAG GAC CTT TGA CCC GAG GGT GAG TCG GGG ACC CTC

100 * 110 * 120 * 130 * 140 *

CAG CAG CCG CCA GCC CCT CGG ACC TCC ATC TCC ACC CTG CTG AGC CAC
GTC GTC GGC GGT CGG GGA GCC TGG AGG TAG AGG TGG GAC GAC TCG GTG

>Sma1 >BamH1

150 | 160 * 170 * 180 * 190 *

CCG GGT TGG GCC AGG ATC CCG GCA GGC TGA TCC CGT CCT CCA CTG AGA
GCC CCA ACC CGG TCC TAG GGC CGT CCG ACT AGG GCA GGA GGT GAC TCT

200 * 210 * 220 * 230 * 240 *

CCT GAA AA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG CAG GAG TGC
GGA CTT TT TAC CGA AGC CCC GTT CGG GGT CCA GGA GGG TCC GTC CTC ACG
M A S G Q G P G P P R Q E C>

250 * 260 * 270 * 280 * 290 *

GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC
CCT CTC GGA CGG GAC GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG
G E P A L P S A S E E Q V A Q D>

300 * 310 * 320 * 330 *

ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC CAT CAG CAG GAA
TGT CTC CTC CAA AAG GCG TCG ATG CAA AAA ATG GCG GTA GTC GTC CTT
T E E V F R S Y V F Y R H Q Q E>

340 * 350 * 360 * 370 * 380 *

CAG GAG GCT GAA GGG GTG GCT GGC CCT GGC GAC CCA GAG ATG GTC ACC
GTC CTC CGA CTT CCC CAC CGA CGG GGA CGG CTG GGT CTC TAC CAG TGG
Q E A E G V A A P A D P E M V T>

>Nco1

390 * 400 * 410 * 420 * 430 *

TIA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC
AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG
L P L Q P S S T M G Q V G R Q L>

440 * 450 * 460 * 470 * 480 *

GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG
CGG TAG TAG CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC

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Figure 3 cont.

A I I G D D I N R R Y D S E F Q>

>Pst1

490 * 500 * 510 * 520 * 530 *

ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC
TGG TAC AAC GTC GTG GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG
T M L Q H L Q P T A E N A Y E Y>

540 * 550 * 560 * 570 *

TTC ACC AAG ATT GCC AOC AGC CTG TTT GAG AGT GGC ATC AAT TGG GGC
AAG TGG TTC TAA CGG TGG TGG GAC AAA CTC TCA CGG TAG TTA ACC CCG
F T K I A T S L F E S G I N W G>

580 * 590 * 600 * 610 * 620 *

CGT GTG GTG GCT CTT CTG GGC TTC GGC TAC CGT CTG GGC CTA CAC GTC
GCA CAC CAC CGA GAA GAC CCG AAG CCG ATG GCA GAC CGG GAT GTG CAG
R V V A L L G F G Y R L A L H V>

630 * 640 * 650 * 660 * 670 *

TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG ACC CGC TTC GTG
ATG GTC GTA CGG GAC TGA CGG AAG GAT CGG GTC CAC TGG GCG AAG CAC
Y Q H G L T G F L G Q V T R F V>

>Sal1

680 * 690 * 700 * 710 * 720 *

GTC GAC TTC ATG CTG CAT CAC TGC ATT GGC CGG TGG ATT GCA CAG AGG
CAG CTG AAG TAC GAC GTA GTG ACG TAA CGG GGC ACC TAA CGT GTC TCC
V D F M L H H C I A R W I A Q R>

730 * 740 * 750 * 760 * 770 *

GGT GGC TGG GTG GCA GGC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC
CCA CCG ACC CAC CGT CGG GAC TTG AAC CGG TTA CCA GGG TAG GAC TTG
G G W V A A L N L G N G P I L N>

780 * 790. * 800 * 810 *

GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG TTT GTG GTA CGA
CAC GAC CAC CAA GAC CCA CAC CAA GAC AAC CGG GTC AAA CAC CAT GCT
V L V V L G V V L L G Q F V V R>

820 * 830 * 840 * 850 * 860 *

AGA TTC TTC AAA TCA TGA C TCC CAA GGG TGC CCT TTG GGT CCC GGT TCA
TCT AAG AAG TTT AGT ACT G AGG GTT CCC ACG GGA AAC CCA GGG CCA AGT
R F F K S *>

>Afl2

870 * 880 * 890 * 900 * 910 *

GAC CCC TGC CTG GAC TTA AGC GAA GTC TTT GGC TTC TCT GTT CCC TTG
CTG GGG ACG GAC CTG AAT TCG CTT CAG AAA CGG AAG AGA CAA GGG AAC

>Hind3

Figure 3 cont.

920 930 940 950 960
 * * * * *
 CAG GGT CCC CCC TCA AGA GTA CAG AAG CTT TAG CAA GTG TGC ACT CCA
 GTC CCA CGG GGG AGT TCT CAT GTC TTC GAA ATC GTT CAC ACG TGA GGT

>Pst1
 970 980 990 1000 1010
 * * * * *
 GCT TCG GAG GCC CTG OGT GGG GGC CAG TCA GGC TGC AGA GGC ACC TCA
 CGA AGC CTC CGG GAC GCA CCC CGG GTC AGT CCG ACG TCT CCG TGG AGT

>Apa1
 1020 1030 1040 1050
 * * * *
 ACA TTG CAT GGT GCT AGT GCC CTC TCT CTG GGC CCA CGG CTG TGG CGG
 TGT AAC GTA CCA CGA TCA CGG GAG AGA GAC CGG GGT CCC GAC ACC GGC

1060 1070 1080 1090 1100
 * * * * *
 TCT CCT CCC TCA GCT CTC TGG GAC CTC CTT AGC CCT GTC TGC TAG GCG
 AGA GGA GGG AGT CGA GAG ACC CTG GAG GAA TCG GGA CAG ACG ATC CGC

1110 1120 1130 1140 1150
 * * * * *
 CTG GGG AGA CTG ATA ACT TGG GGA GGC AAG AGA CTG GGA GCC ACT TCT
 GAC CCC TCT GAC TAT TGA ACC CCT CGG TTC TCT GAC CCT CGG TGA AGA

1160 1170 1180 1190 1200
 * * * * *
 CCC CAG AAA GTG TTT AAC GGT TTT AGC TTT TTA TAA TAC CCT TGT GAG
 GGG GTC TTT CAC AAA TTG CCA AAA TCG AAA AAT ATT ATG GGA ACA CTC

>Aha2
 1210 1220 1230 1240 1250
 * * * * *
 AGC CCA TTC CCA CCA TTC TAC CTG AGG CCA GGA CGT CTG GGG TGT GGG
 TCG GGT AAG GGT GGT AAG ATG GAC TCC GGT CCT GCA GAC CCC ACA CCC

1260 1270 1280 1290
 * * * *
 GAT TGG TGG GTC TAT GTT CCC CAG GAT TCA GCT ATT CTG GAA GAT CAG
 CTA ACC ACC CAG ATA CAA GGG GTC CTA AGT CGA TAA GAC CCT CTA GTC

1300 1310 1320 1330 1340
 * * * * *
 CAC CCT AAG AGA TGG GAC TAG GAC CTG AGC CTG GTC CTG GCC GTC CCT
 GTG GGA TTC TCT ACC CTG ATC CTG GAC TCG GAC CAG GAC CGG CAG GGA

1350 1360 1370 1380 1390
 * * * * *
 AAG CAT GTG TCC CAG GAG CAG GAC CTA CTA GGA GAG GGG GGC CAA GGT
 TTC GTA CAC AGG GTC CTC GTC CTG GAT GAT CCT CTC CCC CCG GTT CCA

1400 1410 1420 1430 1440
 * * * * *
 CCT GCT CAA CTC TAC CCC TGC TCC CAT TCC TCC CTC CGG CCA TAC TGC
 GGA CGA GTT GAG ATG GGG ACG AGG GIA AGG AGG GAG GCC GGT ATG ACG

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Figure 3 cont.

1450 1460 1470 1480 1490
* * * * *
CTT TGC AGT TGG ACT CTC AGG GAT TCT GGG CTT GGG GTG TGG GGT GGG
GAA ACG TCA ACC TGA GAG TCC CTA AGA CCC GAA CCC CAC ACC CCA CCC

1500 1510 1520 1530
* * * *
GTG GAG TCG CAG ACC AGA GCT GTC TGA ACT CAC GTG TCA GAA GCC TCC
CAC CTC AGC GTC TGG TCT CGA CAG ACT TGA GTG CAC AGT CTT CGG AGG

1540 1550 1560 1570 1580
* * * * *
AAG CCT GCC TCC CAA GGT CCT CTC AGT TCT CTC CCT TCC TCT CTC CTT
TTC GGA CGG AGG GTT CCA GGA GAG TCA AGA GAG GGA AGG AGA GAG GAA

1590 1600 1610 1620 1630
* * * * *
ATA GAC ACT TGC TCC CAA CCC ATT CAC TAC AGG TGA AGG CTC TCA CCC
TAT CTG TGA ACG AGG GTT GGG TAA GTG ATG TCC ACT TCC GAG AGT GGG

1640 1650 1660 1670 1680
* * * * *
ATC CCT GGG GGC CTT GGG TGA GTG GCC TGC TAA GGC TCC TCC TTG CCC
TAG GGA CCC CCG GAA CCC ACT CAC CGG ACG ATT CCG AGG AGG AAC GGG

1690 1700 1710 1720 1730
* * * * *
AGA CTA CAG GGC TTA GGA CTT GGT TTG TTA TAT CAG GGA AAA GGA GTA
TCT GAT GTC CCG AAT CCT GAA CCA AAC AAT ATA GTC CCT TTT CCT CAT

1740 1750 1760 1770
* * * *
GGG AGT TCA TCT GGA GGG TTC TAA GTG GGA GAA GGA CTA TCA ACA CCA
CCC TCA AGT AGA CCT CCC AAG ATT CAC CCT CTT CCT GAT AGT TGT GGT

>BamH1

1780 1790 1800 1810 1820
* * * * *
CTA GGA ATC CCA GAG GTG GAT CCT CCC TCA TGG CTC TGG CAC AGT GTA
GAT CCT TAG GGT CTC CAC CTA GGA GGG AGT ACC GAG ACC GTG TCA CAT

1830 1840 1850 1860 1870
* * * * *
ATC CAG GGG TGT AGA TGG GGG AAC TGT GAA TAC TTG AAC TCT GTT CCC
TAG GTC CCC ACA TCT ACC CCC TTG ACA CTT ATG AAC TTG AGA CAA GGG

1880 1890 1900 1910 1920
* * * * *
CCA CCC TCC ATG CTC CTC ACC TGT CTA GGT CTC CTC AGG GTG GGG GGT
GGT GGG AGG TAC GAG GAG TGG ACA GAT CCA GAG GAG TCC CAC CCC CCA

1930 1940 1950 1960 1970
* * * * *
GAC AGT GCC TTC TCT ATT GGC ACA GCC TAG GGT CTT GGG GGT CAG GGG
CTG TCA CGG AAG AGA TAA CCG TGT CGG ATC CCA GAA CCC CCA GTC CCC

1980 1990 2000 2010
* * * *

GGA GAA GTT CTT GAT TCA GCC AAA TGC AGG GAG GGG AGG CAG ATG GAG
CCT CTT CAA GAA CTA AGT CGG TTT ACG TCC CTC CCC TCC GTC TAC CTC

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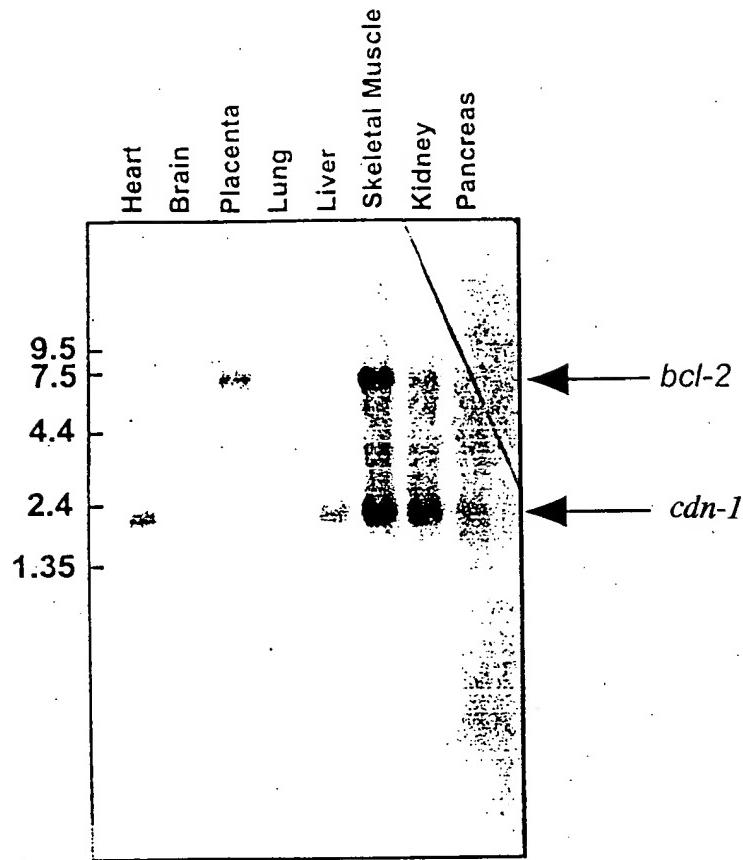
Figure 3 cont.

2020	2030	2040	2050	2060
*	*	*	*	*
CCC ATA GGC CAC CCC CTA TCC TCT GAG TGT TTG GAA ATA AAC TGT GCA GGG TAT CCG GTG GGG GAT AGG AGA CTC ACA AAC CTT TAT TTG ACA CGT				
2070	2080	2090		
*	*	*		
ATC CCC TCA AAA AAA AAA CGG AGA TCC TAG GGG AGT TTT TTT GCC TCT AGG				

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Figure 4

Multiple Tissue Northern
bcl-2 and cdn-1 hybridization



Random primed, Klenow-labeled fragments of *bcl-2* and *cdn-1* clones were hybridized to a multiple human tissue Northern blot (Clontech 7760-1), at a final concentration of 1×10^6 cpm/ml for each probe. Blot was washed at high stringency.

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Figure 5 cdn-2 gene sequence

10	20	30	40	50	60
*	*	*	*	*	*
TTT TAA TAT AAA TTA ATG TGC TCT ATT TAT AGA GAC AAT ACA TGA AAT ATA CTT AAT AAA AAA ATT ATA TTT AAT TAC ACG AGA TAA ATA TCT CTG TTA TGT ACT TTA TAT GAA TTA TTT					
70	80	90	100	110	120
*	*	*	*	*	*
AAT TCA AAT GTT ATA GAA CTG AAA AAG ATG AAA AGT AAA AAC AAC CTA TTC CCC AGA GGT TTA AGT TTA CAA TAT CTT GAC TTT TTC TAC TTT TCA TTT TTG TTG GAT AAG GGG TCT CCA					
130	140	150	160	170	180
*	*	*	*	*	*
AGC CAC TGT CCA TAG TTT CTA TTT TAG ATT CTT TCC TTT ATA CAA GAT TAT TAT AGC TTC TCG GTG ACA GGT ATC AAA GAT AAA ATC TAA GAA AGG AAA TAT GTT CTA ATA ATA TCG AAG					
190	200	210	220	230	240
*	*	*	*	*	*
TAT TTT TTG GTG TAT GAA CTG TAG TCC TAG AGG ATT TTA TTA GTT ATG AGT TCT ATA ACT ATA AAA AAC CAC ATA CTT GAC ATC AGG ATC TCC TAA AAT AAT CAA TAC TCA AGA TAT TGA					
250	260	270	280	290	300
*	*	*	*	*	*
AAG ATC CAT CAT CTT AGT TGC TAA GAA CGT AGA TAC TGA GAA CAT CAT TTA AAA AAA CAT TTC TAG GTA GTA GAA TCA ACG ATT CTT GCA TCT ATG ACT CTT GTA ATA AAT TTT TTT GTA					
310	320	330	340	350	360
*	*	*	*	*	*
TTT TGG CTG GCA CCT CAT GAT CAC TGG AGT CTC GCG GGT CCC TCA GGC TGC ACA GGG ACA AAA ACC GAC CGT GGA GTA CTA GTG ACC TCA GAG CGC CCA GGG AGT CCG ACG TGT CCC TGT					
370	380	390	400	410	420
*	*	*	*	*	*
AGT AAA GGC TAC ATC CAG ATG CTG GGA ATG CAC TGA CGC CCA TTC CTG GAA ACT GGG CTC TCA TTT CCG ATG TAG GTC TAC GAC CCT TAC GTG ACT GCG GGT AAG GAC CTT TGA CCC GAG					
430	440	450	460	470	480
*	*	*	*	*	*
CCA CTC AGC CCC TGG GAG CAG CAG CCG CCA GCC CCT CGG GAC CTC CAT CTC CAC CCT GCT GGT GAG TCG GGG ACC CTC GTC GGC GGT CGG GGA GCC CTG GAG GTA GAG GTG GGA CGA					
>BamHI					
490	500	510	520	530	540
*	*	*	*	*	*
GAG CCA CCC GGG TTG GGC CAG GAT CCC GGC AGG CTG ATC CCG TCC TCC ACT GAG ACC TGA CTC GGT GGG CCC AAC CCG GTC CTA GGG CCG TCC GAC TAG GGC AGG AGG TGA CTC TGG ACT					
550	560	570	580	590	600
*	*	*	*	*	*
AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA GAG CCT GCC CTG TTT TAC CGA AGC CCC GTT CCG GGT CCA GGA GGG TCC GTC CTC ACG CCT CTC GGA CGG GAC					
M	A	S	G	P	L>
			Q	G	
				P	
				R	
				Q	
				E	
				C	
				G	
				E	
				P	
				A	
610	620	630	640	650	660
*	*	*	*	*	*
CCC TCT GCT TCT GAG GAG CAG GTC GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT GGG AGA CGA AGA CTC CTC GTC CAT CGG GTC CTG TGT CTC CTC CAA AAG GCG TCG ATG CAA					
P	S	A	S	E	V>
				Q	
				V	
				A	
				Q	
				E	
				A	
				E	
				G	
				A	
				A	
				A	
				P	
				A	
				D	
				P	
				E	
670	680	690	700	710	720
*	*	*	*	*	*
TTT TAC CAC CAT CAG CAG GAA CAG GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG AAA ATG GTG GTA GTC GTC CTT GTC CTC CGA CTT CCC CGC CGA CGG GGA CGG CTG GGT CTC					
F	Y	H	H	Q	E>
				Q	
				E	
				A	
				E	
				G	
				A	
				A	
				A	
				P	
				A	
				D	
				P	
				E	

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Figure 5 cont.

>Nco1

730	740	750	760	770	780
*	*	*	*	*	*
ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC	TAC CAG TGG AAT GGA GAC GTT GGA TCG TCG TGG TAC CCC GTC CAC CCT GCC GTC GAG CGG	M V T L P L Q P S S T M G Q V G R Q L A>			
790	800	810	820	830	840
*	*	*	*	*	*
ATC ATT GGG GAC GAC ATC AAC CGA CGC TAT GAC TCA GAG TTC CAG ACC ATG TTG CAG CAC	TAG TAA CCC CTG CTG TAG TTG GCT GCG ATA CTG AGT CTC AAG GTC TGG TAC AAC GTC GTG	I I G D D I N R R Y D S E F Q T M L Q H>			

>Pst1

850	860	870	880	890	900
*	*	*	*	*	*
CTG CAG CCC ACG GCA GAG AAT GCC TAT GAG TAC TTC ACC AAG ATT GCC TCC AGC CTG TTT	GAC GTC GGG TGC CGT CTC TTA CGG ATA CTC ATG AAG TGG TTC TAA CGG AGG TCG GAC AAA	L Q P T A E N A Y E Y F T K I A S S S L F>			
910	920	930	940	950	960
*	*	*	*	*	*
GAG AGT GGC ATC AAT TGG GGC CGT GTG GCT CTT CTG GGC TTC AGC TAC CGT CTG GCC	CTC TCA CCG TAG TTA ACC CCG GCA CAC CGA GAA GAC CCG AAG TCG ATG GCA GAC CGG	E S G I N W G R V V A L L G F S Y R L A>			
970	980	990	1000	1010	1020
*	*	*	*	*	*
CTA CAC ATC TAC CAG CGT GGC CTG ACT GGC TTC CTG GGC CAG GTG ACC CGC TTT GTG GTG	GAT GTG TAG ATG GTC GCA CCG GAC TGA CCG AAG GAC CCG GTC CAC TGG GCG AAA CAC CAC	L H I Y Q R G L T G F L G Q V T R F V V>			
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG ATT GCA CAG AGG GGT GGC TGG GTG GCA	CTG AAG TAC GAC GTA GTG ACG TAA CGG GCC ACC TAA CGT GTC TCC CCA CCG ACC CAC CGT	D F M L H H C I A R W I A Q R G G W V A>			
1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
GCC CTG AAC TTG GGC AAT GGT CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG	CGG GAC TTG AAC CCG TTA CCA GGG TAG GAC TTG CAC GAC CAC CAA GAC CCA CAC CAA GAC	A L N L G N G P I L N V L V V L G V V L>			
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
TTG GGC CAG TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTC CCA AGG GTG CCT TTG GGG	AAC CCG GTC AAA CAC CAT GCT TCT AAG AAG TTT AGT ACT GAG GGT TCC CAC GGA AAC CCC	L G Q F V V R R F F K S *>			
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
TCC CAG TTC AGA CCC CTG CCT GGA CTT AAG CGA AGT CTT TGC CTT CTC TGC TCC TTG CAG	AGG GTC AAG TCT GGG GAC GGA CCT GAA TTC GCT TCA GAA ACG GAA GAG ACG AGG AAC GTC				

>Hind3

1270	1280	
*	*	
GGT CCC CCC TCA AGA GTA CAG AAG CTT	CCA GGG GGG AGT TCT CAT GTC TTC GAA	

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Figure 6 Amino acid sequences of cdn-1,cdn-2, and bcl-2 family proteins

Figure 7

cdn-3 enzyme cDNA sequence

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QUAPTCGCGT AATAGTAA AGAACGGA ACUAGCTGT TGTCTCTCT GAGTCACG TCTCTCTCA AAAATGCGA
 60
 ADATTTGTA AGACTCCGTA AAAATCTAC GACTCAGAA GAGGCAATG CGGACTGCG AGAGAGAGA CGCTTGAGAA
 120
 ACACACAGA CTGGTTTAG ATTCCTCAC TCCACOCATG GTGTCAGTC CGCAACATC TGCACCTTC TAAADGCCA
 180
 TCTGTGATC TGACAGGA TGAATGAGA ATGATGATCA CGCAACATG CGAAATGCA CGTAAAGA TGGCTGCG
 240
 TTTCCTACTA AAATGCTCA CGCCATCA TCTACGAA AAACGCTCG TGTCTCTTC TTAAGGCTAT TGCTGCGATG
 300
 TGTTTACCG GAACGCTAG CGTTCCTCA CGCAACATC CGCAGCGCT CGCAAAATG CGACACGCT TCAEGGATG
 360
 TGTCTGATG AGACACGCTG CCGTCACAT CGGCGCGCT AGCTAGATG GATTCCTGAG CGCCATTAG CGGGGGATA
 420
 CGACATGCC ACCACATCA CGATTTCTG CGACACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 480
 GAGCTGAGG CGACACGCG AGACACGCT CGCAACATC CGTTCCTCA AGCGCGACG CGCCATTAG CGGGGGATA
 540
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 600
 CGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 660
 CGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 720
 GAGCTGAGG CGACACGCG AGACACGCT CGCAACATC CGTTCCTCA AGCGCGACG CGCCATTAG CGGGGGATA
 780
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 840
 CGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 900
 CGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 960
 CGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1020
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1080
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1140
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1200
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1260
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1320
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1380
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1440
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1500
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC
 1560
 CGCTGAGG AGACACGCT CGACACGCT CGCAACATC AGCGCGACG ATTCCTCTC AAATGATAAT CGCTAACAC

Figure 7 cont.

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TCAGGCAAGC CGCTTGCAC AGCATCGTG GAGCTGCA CGTGTGCGA CTAGAGCGC AAAA ATG OCA TGG CGG
N A S Q>

1680

CTA CCC CCA DOG OCT CCC ADC CAD GAC TGC CGA MAG CTT GCT CGG DCC TCT GCT TGT TGT GAG GAG CAG
R C P Q P P R D B C O E F A L P S A B X E Q>

1760

GTA CGC CAG GAC ATG GAG CGG TIT TCC OCA OCT ADC TTT TTT ACC ACC ATC ACC AGG AAC AGG AGG
Y A Q D H E G P S A A T F F T I S R H R R>

1840

TGG AAB CGG CGG CGG DCC CTC CGG ACC CAD AGA TGG TCA CCT TGC CCC TCC AAC CTA OCA CGA OCA
L K G R P P L P T Q R W S P C P S X L A A P>

1920

TGG CGC AGG TGG GAC CGC ADC TGG CGA TCA OCA CGA CGA CAT CAD CGG GCA CTA TGA CGT CGG AGT
W G R H D G S S P S P G B H Q P A L >

2000

TCAGGACAT CGTGCAGGAC CTUGACGCCA CGCAGAGAA CGCTGAGAG PACTGCGCA AGATCGCTC CGTCGCTT

2080

CAGAGTCGCA TCAUCGCGG CGCTGCTTG CGTCCTCTTG CGTCGGCTA CGTCGCTC CGTCGCTC ACCAGCAAC

2160

CTTCAGCTGC CGTCGCGCC TGGTGACCCG CTTCGCGTC CGTCGCTC AACAGGCGAT CGCCCGGCGT ATCTCGACA

2240

CGGCGGGCGT CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2320

CGGCGGGCGT CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2400

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2480

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2560

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2640

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2720

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2800

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2880

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

2960

ATACTGCGT CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

3040

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

3120

CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC CGTCGCTGC

Figure 7 cont.

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ACCGCGCAGA CTGACGGCTT TGTTCACCG CGTGTTTCG TATTCACCG AGAAAGCTTA CGGAGCTAT CTCGAGCTT
 3200
 CTACTGCGA CAGGAGCTT CAAGCAGA CGAACTCCAG AGGTGGCCATC CTGGCTTCAAG CGCTGGCGAC AGCTTAATCC
 3280
 ACGGGGAG ATACGGAACT CGAAAGCTT GAACTGTTG CGGGGACCTT CGAAGCTCC GACCTTCTG CGCTCTCTCT
 3360
 CGTCGTTGG CGGAGGCTTC CTTCCTTATC CGGCACGCC TAGGGCTTC CGGCTGAAGG CGGAGGAGCTT CTGGATTCAG
 3440
 CGAAATGCCG CGGAGGAGG CGAAAGGAG CGAACGCCA CTGGCTATCC TCTGAGTTT TGGAAATAAA CGCTGCGATC
 3520
 CGTCGTTGG CGGAGGAGG CGAAAGGAG CGAACGCCA CTGGCTATCC TCTGAGTTT TGGAAATAAA CGCTGCGATC
 3600
 CGTCGTTGG CGGAGGAGG CGAAAGGAG CGAACGCCA CTGGCTATCC TCTGAGTTT TGGAAATAAA CGCTGCGATC
 3680
 CTTCATGAC ACAAACCTAC AGTTAGAGG TAAAGATAG TCTGGTGCAC CGACCGGCC CGACACCTCT AACCTCCACCA
 3760
 CTITGGAGA CGAAAGGAGG CGAAAGGAG CGAACGCCA CTGGCTATCC TCTGAGTTT TGGAAATAAA CGCTGCGATC
 3840
 TACGAGAT TTAAGAAA CGAAAGGAGG CGAACGCCA CTGGCTATCC CGGAGGCTTA CGGGGGAGAA
 3920
 TCTGGAGAC CGGGGATTAA CGAAAGGAGG CGAACGCCA CTGGCTATCC TCTGAGTTT TGGAAATAAA CGCTGCGATC
 4000
 CGACCTGCTT CAAGATAAA CGGGGACAA GTCTAGTTT TCTATGCCCG AAATGGGTA CGGGGGTAG CGAACGCCA
 4080
 TTGGGTTT CAAGATAAA CGGGGACAA GTCTAGTTT TCTATGCCCG AAATGGGTA CGGGGGTAG CGAACGCCA
 4160
 CGGGGGATG CGGGGGATG ATCATTCAC ACCTCAATGTA TCTATGCCCG AAATGGGTA CGGGGGTAG CGAACGCCA
 4240
 TCTATGCCCG AAATGGGAG CGGGGGATG CGGGGGATG CGGGGGTAG CGAACGCCA
 4320
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGTAG CGAACGCCA
 4400
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGTAG CGAACGCCA
 4480
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGTAG CGAACGCCA
 4560
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG
 4640
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG
 4720
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG
 4800
 CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG CGGGGGATG

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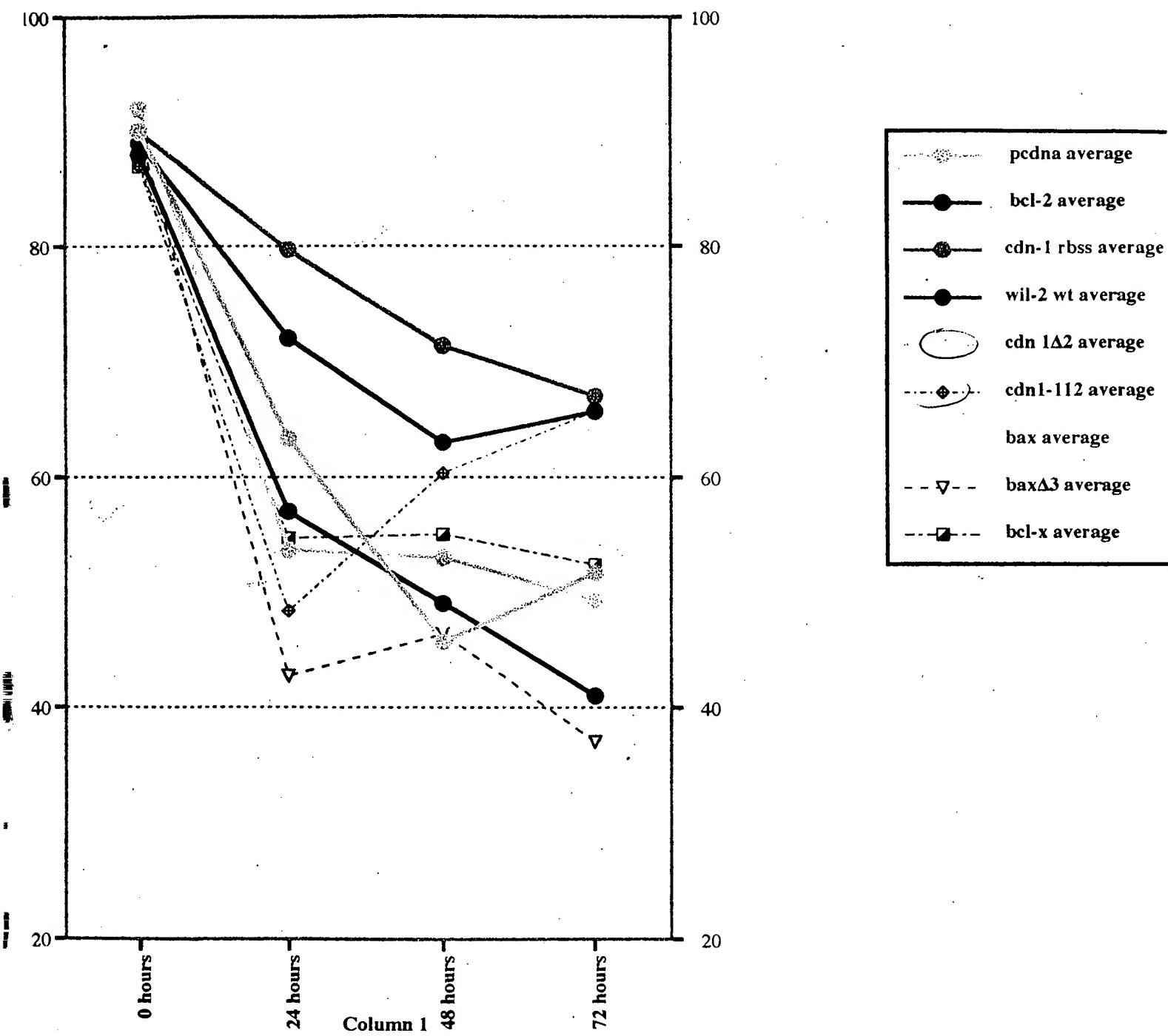
Figure 7 cont.

6880
GTTTCAGACCC ATCATGCCA ACATGGCAA ACCGGATCTC TGTCAAAAT AGAAAATA CCCTGGCTG GTCGGCGCA
6960
CTCTGAGTGC CAGCTACTCC CGACCGTGAC CGAGGAAAT CCTTGAGCC TGGGGCCCG AGGTTGACTG GACCGATA7
5010
CAGGCGACTG CACTGGACCC TGGGGACAGA CGGAGACTCC ATCTGAAAAA AAGGAAAGA TAAATGCTTG AAAFAAACAC
5120
TGGCGATAA GAGGAAAGA AGTTTATAA AGTGAAGA TAAAGTAAA AACGGCTCC AGGCTGATT CGCGCGAGC
5200
GCTGTGGAC ACAGACCCCG AGCGATGAC TTCAAAATC CGCTGGTAAG TCAAGCTCAC CTGGGTTTTT CGGGACCGA
5280
CTCACTTTAA AACAGTTGCC TGGATTCTRA CCTTAACCCAG AAGATCAGAC TCTTGTACCT AAATTCCTAA CCTCCCTGG
5360
GATGATGAGG GAAACGTTTT ATGGCTGACG CGAGCTACG CTCTGAAGA CCTGGCGAT AGCTCTCTG CGACGCTCCC
CTTCGCTOC ATGGCCCGGG GATGATTC

Wil-2 transformants 0.1% FBS

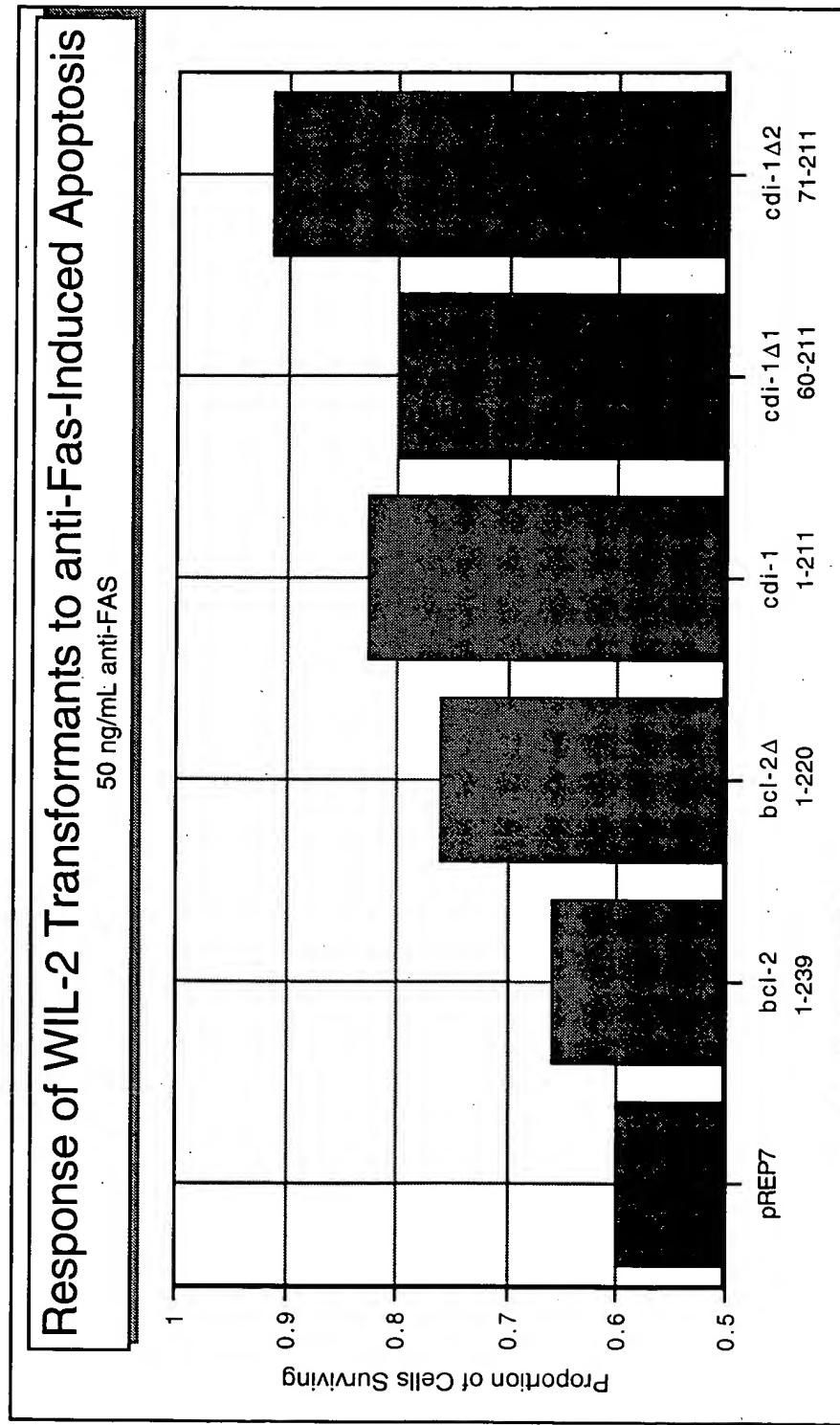
Figure 8

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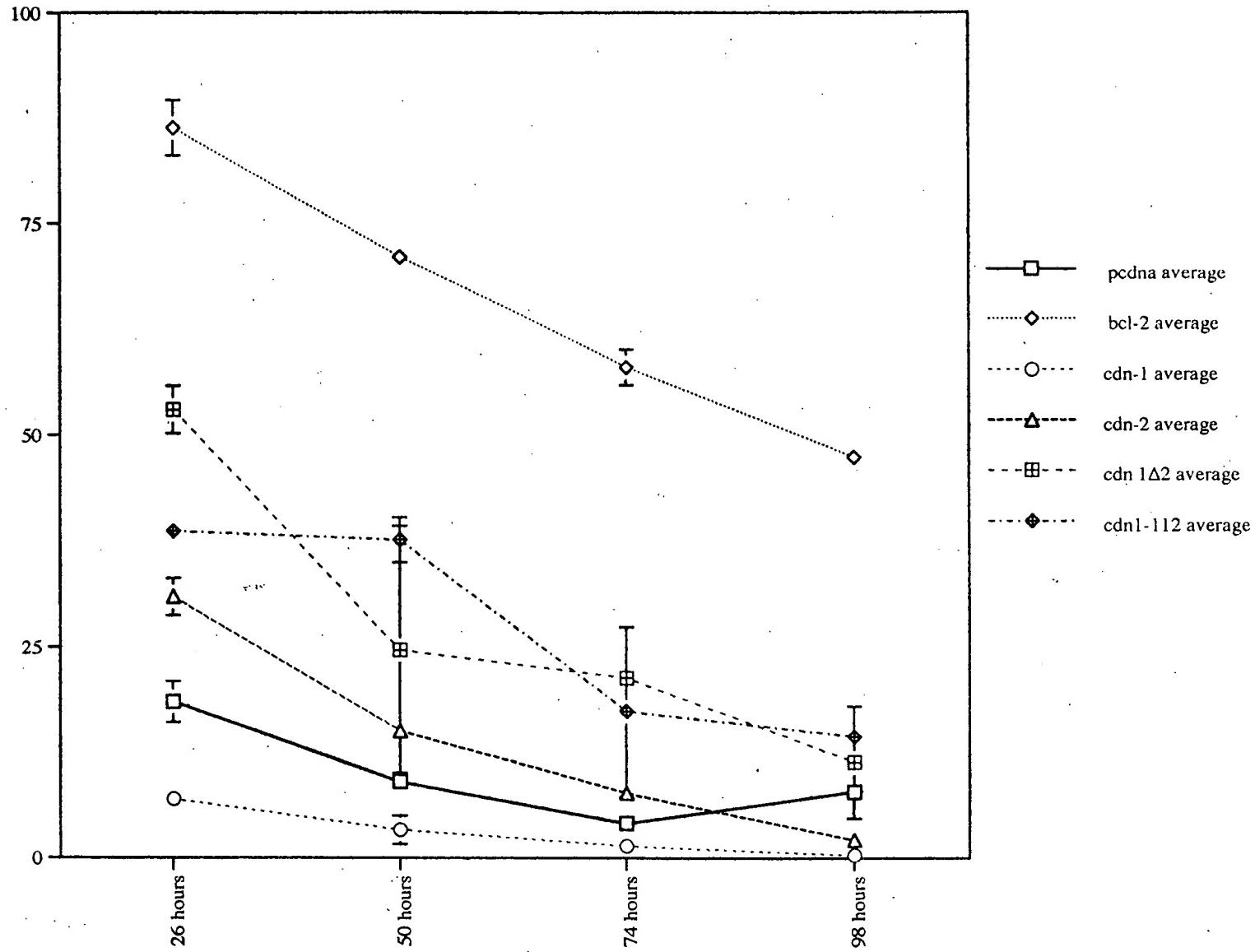
Figure 9



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Figure 10

F15.12 transformants - IL-3



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Figure 11 N-terminal methionine residues of cdm-1 derivatives

Δ_1 MASGQGPPRQECCGEPALPSASEEQVAQDTEEVRSYVFRHQEQEAEQVAAPADPEMVT
 Δ_2 LPLQPSSTMQVGRLAIIIGDDINRRYDSEFORTMLQHLOPTAENAYEFTKIASTSFLFESGNWGRVVALLGFGYRLALHVYQHGLTGFGLGVTRVVDFMLIH
 Δ_3 CIARWIAORGGWVAALNLNGNPGILNVLVLGVLLGOFVVRFFKS